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Microbial N cycling functional gene abundance in forage grazed pasture soils and links to N_2O emissions

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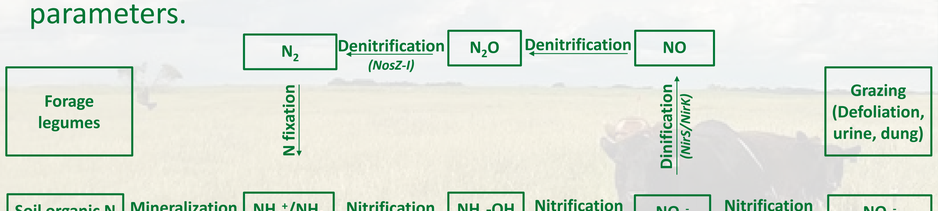
SOILS & CROPS

INTRODUCTION

- Non-bloat legumes (such as Cicer milkvetch (*Astragalus cicer L.*) or Sainfoin (*Onobrychis vicifolia*) are potential alternatives for alfalfa (*Medicago sativa L.)* in forage grazing pastures
- Introduction of the new legumes complicates microbial N cycling and the link to N_2O under these systems.
- Information on N_2O emissions from soil and N functional gene abundance in semi-arid grassland is limited.

OBJECTIVES

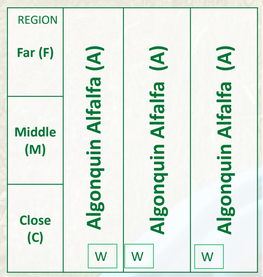
- Characterize N functional gene abundance in soils under different grass-legume grazing pasture.
- Investigate the relationships among bloat and non-bloat legumes, N_2O emissions, N-related soil chemical and microbiological parameters.



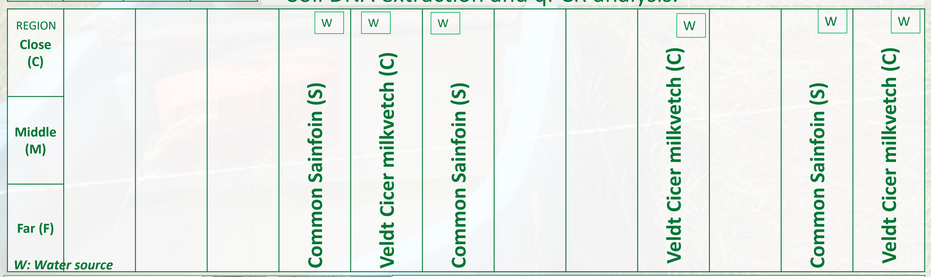
amoA: Ammonia monooxygenase subunit alpha ; *AOB*: Ammonia-oxidizing bacteria;
NirS: Cytochrome cd1 version Nitrite-reductase; *NirK:* Copper Nitrite-reductase; *NosZ-I:* Nitrous oxide reductase, clade I.

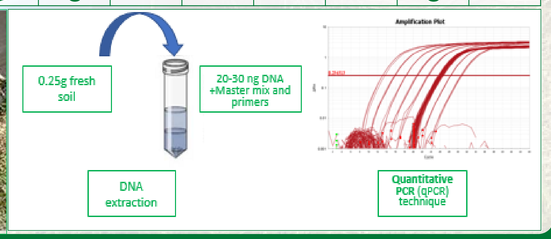
Diagram 1: Microbial N cycling and key N functional genes in soils under grazed forage legume pasture

MATERIALS AND METHODS



- Termuende Research Farm, Lanigan, SK.
- Established grass/Algonquin Alfalfa stand (Control), sod seeded non-bloat legumes (Common Sainfoin, Veldt Cicer milkvetch) x 3 replicate grazed paddocks (65 x 300m x 4-5 steers/year)
- Soil N_2O flux chambers.
- Soil samples (0-10 cm): 3 regions x 9 paddocks x single timepoint (August) x 2 years (2017, 2018)
- Soil DNA extraction and qPCR analysis.





RESULTS

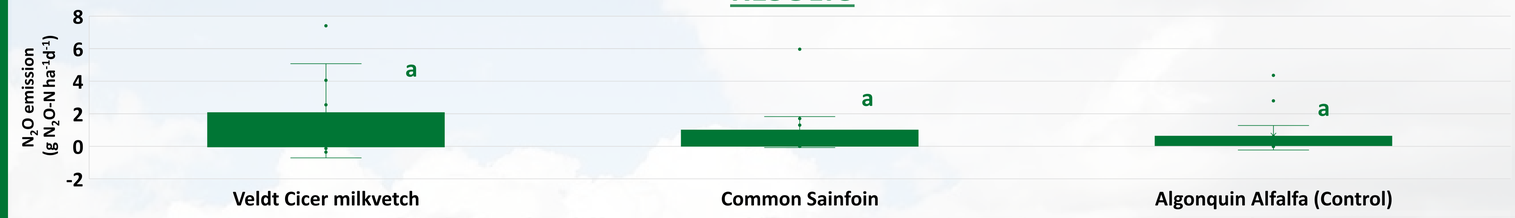


Figure 1: N_2O emission under different grazed legume-grass mixture in August, 2017 and 2018

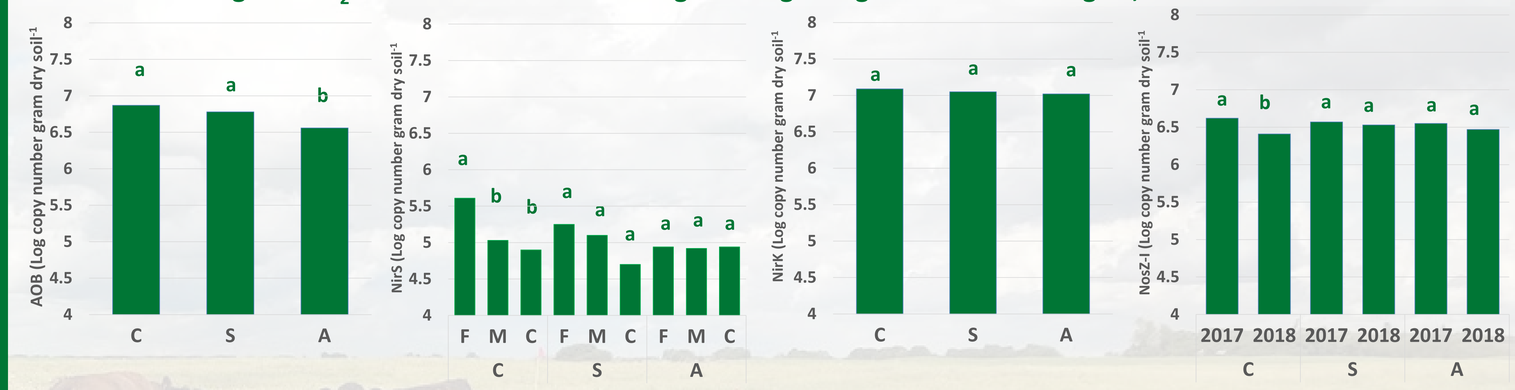
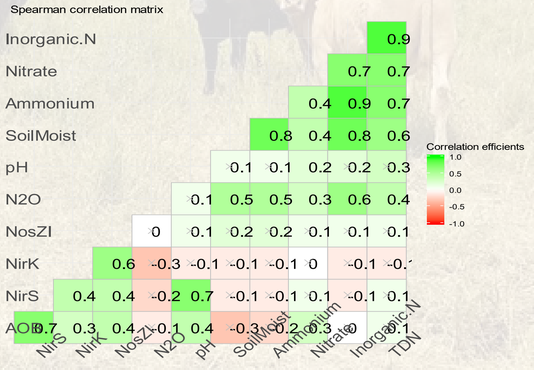
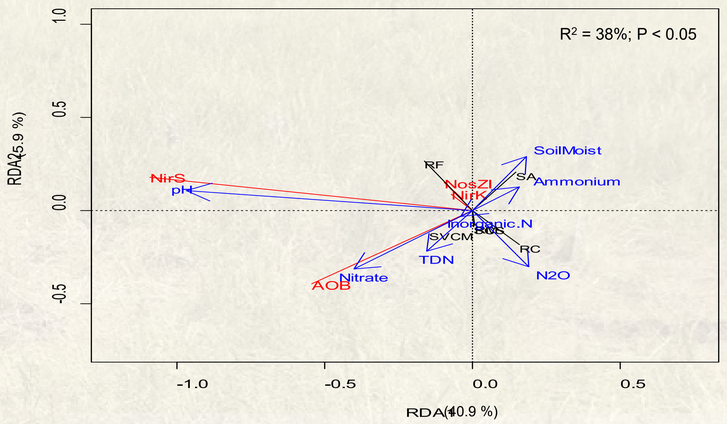


Figure 2: N functional gene abundance in soils under different grazed legume-grass mixture in August, 2017 and 2018



Covariation efficiencies with "X"symbol are non-significant (P > 0.05).
TDN: Total disovled organic nitrogen.

Figure 3: Correlation among N functional gene abundance, N_2O emissions and N-related soil parameters



RF: Region-Far; RM: Region-Middle; RC: Region-Close.
SVCM: Species-Velt Cicer Milkvetch; SCS: Species-Common Sainfoin; SA: Species-Alfalfa.

Figure 4: RDA biplot among explanatory variables (species, region), N functional gene abundance, N_2O emissions and N-related soil parameters

MAIN FINDINGS, DISCUSSION AND CONCLUSION

- Despite no difference in N_2O emission under different grass-legume mixtures (Fig.1), *AOB* gene abundance was higher in non-bloat grass pasture soils (Fig.2), indicating a potential nitrification (by bacteria) under these pasture.
- In Cicer milkvetch: There were (i): a *species x region* interaction effect on *NirS* gene abundance, which was more abundant in the far region - the most crowded area; (ii) a *year x species* interaction effect on *NosZI* abundance in 2018-a drier year (Fig.2), which suggest a key role of grazing density and water on these denitrifiers.
- Gene abundance (*AOB, NirS/K, NosZI*) was not correlated to N_2O, but *AOB* and *NirS* were correlated with soil pH (Fig.3).
- Soil pH as well as *AOB, NirS* gene abundance were positively associated with Cicer milkvetch, might be potential predictors for N cycling in soil under this pasture.

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